

Project Report: Bacterial tubulin and its implications on the evolution of Eukaryotes

Project Investigator:

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Project Progress

During the past year we have focused on determining whether the bacterium, *Prostheco bacter dejongeeii* , which has alpha- and beta-tubulin analogues previously found only in eukaryotic organisms, contain other eukaryotic proteins. To carry out this work, we compared the genome of *P. dejongeeii* with 347 Eukaryotic signature proteins (ESP) from a published list. In addition to *P. dejongeeii*, two additional bacteria were included as control organisms, *Gemmata* Wa-1 of the Planctomycetes phylum and *Caulobacter crescentus* of the Proteobacteria. The protist, *Trypanosoma brucei* , was used as a eukaryotic control. *Prostheco bacter dejongeeii* had unique ERGO blast matches to alpha-, beta-, and gamma-tubulin, Set2, a transcriptional factor associated with eukaryotic DNA, and LAMMER protein kinase for a total of 12 high ESP matches altogether. *Gemmata* Wa-1 shared six of its 19 high ESP matches with *P. dejongeeii* , and that information coupled with other genomic data provide strong support that these two phyla are related to one another. If the ESP list is an accurate listing of unique eukaryotic proteins, the low number of high matches between the proteins of these two bacteria with the list raise strong doubts about these organisms being direct ancestors of the Eucarya. However, this does not rule out the possibility that ancestral members of either the Verrucomicrobia or Planctomycetes may have played a role in the evolution of a Proto-eukaryotic organism.

We are also continuing our study of Bacteria and Archaea from desert varnish by use of sequence analyses of 16S rDNA obtained from DNA extracts of desert varnish. The dark varnish is an analogue for possible rock coatings found on Mars and other extra-terrestrial environments. The main question we are addressing is: Do biological signatures indicative of varnish coatings occur on Earth? Samples analyzed to date provide evidence that members of both the Bacteria and Archaea occur in the rock coatings.

Roadmap Objectives

- **Objective No. 3.2: Origins and evolution of functional biomolecules**

Cross Team Collaborations

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